Claims 1, 4, 6-7, 10-12, and 15-17 have been amended and claims 8-9, 13-14, and 18-26 have been cancelled without prejudice or disclaimer to the underlying subject matter. New claims 27-35 have been added. Support for the new claims and the amendments is found throughout the specification, the original claims, the figures and sequence listing, *e.g.* at page 3 line 25 to page 5 line 23, page 11 lines 17-25, page 96 line 28, and page 147 line 34. No new matter enters by these amendments. The application presently contains claims 1-5, 7, 10-12, 15-17, and 27-35.

The Examiner required restriction to one of the following inventions under 35 U.S.C. § 121:

Group I: Claims 1-17, drawn to methods of isolating a region of genomic DNA associated with a phenotype of interest, classified in class 6, subclass 6 with a selection of a single polymorphism.

Group II: Claims 18-23, drawn to a collection of non-identical nucleic acid molecules, classified in class 536, subclass 24.3 with a selection of a group of polymorphisms.

Group III: Claim 24, drawn to a computer medium, classified in class 702, subclass 19 with a selection of a group of polymorphisms.

Group IV: Claim 25, drawn to a method of introgressing a trait, classified in class 800, subclass 278 with a selection of a single polymorphism.

Group V: Claim 26, drawn to a method of identifying transposons, classified in class 435, subclass 6.

Applicants respectfully submit that the restriction requirement is inappropriate because the complete examination of the application would be handled most expeditiously by treating all of the pending claims as a single entity. However, to facilitate prosecution, Applicants have elected Group I, and cancelled claims that do not correspond to Group I.

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Applicants thank the Examiner for her agreement that prosecution would be facilitated by the election of two polymorphisms from Table A. Applicants have amended claims 6 and 11 to recite Single Nucleotide Polymorphism 466799, and claims 7 and 12 to recite Single Nucleotide Polymorphism 471736. Again, to facilitate prosecution, Applicants note that Cho, *et al.* (previously made of record) reports a polymorphism with the following sequence:

GCAGAGGGTATGGCATTGTT (c/a) TGTATCTTGTTCCACACAAA.

Concurrently with this preliminary amendment, Applicants are submitting a Supplemental Information Disclosure Statement and PTO 1449 citing articles which refer, at least in part, to a public release of high density polymorphic markers in *Arabidopsis*.

The presently pending claims are believed to be in immediate condition for allowance. Accordingly, the Examiner is respectfully requested to pass this application to issue. The Examiner is invited to contact Applicants' undersigned representative at 202.942.5068 to address any unresolved issues remaining in this application.

The U.S. Patent and Trademark Office is hereby authorized to charge any fee deficiency, or credit any overpayment, to our Deposit Account No. 50-1824, referencing matter number 16517.127. Again, Applicants thank the Examiner for the August 16, 2001 interview.

Respectfully submitted,

David R. Marsh (Reg. No. 41,408)
June E. Cohan (Reg. No. 43,471)

Date: 16 November 2001

ARNOLD & PORTER
555 Twelfth Street, N.W.
Washington, D.C. 20004-1206
202.942.5000 telephone
202.942.5999 facsimile

I hereby certify that the foregoing Preliminary Amendment is being facsimile transmitted to the attention of Juliet Einsmann, via facsimile number (703) 740-5142.

June E. Cohan   November 16, 2001
                                 Date

Marked-Up Claims

1.   (Once Amended) A method of isolating a region of genomic DNA associated with a phenotype of interest comprising:

(A) identifying an *Arabidopsis* plant of a first ecotype with a phenotype of interest;

(B) crossing said *Arabidopsis* plant with an *Arabidopsis* plant of a second ecotype lacking said phenotype;

(C) propagating and self pollinating seeds from said cross;

(D) selecting progeny of self pollinated seeds with said phenotype;

(E) screening progeny of self pollinated seeds with said phenotype with a collection of nucleic acid molecules, said collection of nucleic acid molecules capable of detecting a set of polymorphisms where the polymorphisms are distributed throughout the genome of said self pollinated seeds with said phenotype at an average density of more than one polymorphism per about 100kb[, wherein at least one of the polymorphisms is selected from Table A];

(F) calculating the linkage of each of said polymorphisms to said phenotype; and

(G) isolating said region of genomic DNA associated with said phenotype based on its linkage to one or more of said nucleic acid molecules.

4.   (Once Amended) A method of identifying a region of genomic DNA associated with a phenotypic trait of interest comprising:

(A)   screening a mapping population of *Arabidopsis* plants to determine the linkage of said phenotypic trait with a collection of nucleic acid molecules, wherein said nucleic acid molecules are capable of detecting a set of polymorphisms, where the polymorphisms are distributed throughout the genome of said mapping population of *Arabidopsis* plants at an

average density of more than one polymorphism per about 100kb[, wherein at least one of the

polymorphisms is selected from Table A];

(B)   calculating the linkage of each of said polymorphisms to said phenotypic trait; and

(C)   identifying said genomic DNA region associated <u>with</u> said phenotypic trait based

on its linkage to one or more of said nucleic acid molecules.

6.   (Once Amended) The method of identifying a region of genomic DNA associated

with a phenotypic trait of interest according to claim 4, wherein said collection of nucleic acid

molecules is capable of detecting [a set of greater than 25 polymorphisms selected from Table A]

<u>Single Nucleotide Polymorphism 466799</u>.

7.   (Once Amended) The method of identifying a region of genomic DNA associated

with a phenotypic trait of interest according to claim [6] <u>4</u>, wherein said collection of nucleic

acid molecules is capable of detecting [a set of greater than 50 polymorphisms selected from

Table A] <u>Single Nucleotide Polymorphism 471736</u>.

10.   (Once Amended) A method of [identifying] <u>isolating</u> a nucleic acid molecule

associated with a phenotypic trait of interest comprising:

(A)   screening a mapping population of *Arabidopsis* plants to determine the linkage of

said phenotypic trait with a collection of polymorphisms, wherein said polymorphisms are

distributed throughout the genome of said mapping population of *Arabidopsis* plants at an

average density of more than one polymorphism per about 100kb[, wherein at least one of the

polymorphisms is selected from Table A];

(B)   calculating the linkage of each of said polymorphisms to said phenotypic trait;

and

(C)   isolating said nucleic acid molecule associated with said phenotypic trait based on its linkage to one or more of said polymorphisms.

11.   (Once Amended) The method of [identifying] isolating a nucleic acid molecule associated with a phenotypic trait of interest according to claim 10, wherein said collection of polymorphisms is capable of detecting Single Nucleotide Polymorphism 466799 [comprises at least 25 polymorphisms selected from Table A].

12.   (Once Amended) The method of [identifying] isolating a nucleic acid molecule associated with a phenotypic trait of interest according to claim [11] 10, wherein said collection of polymorphisms is capable of detecting Single Nucleotide Polymorphism 471736 [comprises at least 50 polymorphisms selected from Table A].

15.   (Once Amended) The method of [identifying] isolating a nucleic acid molecule associated with a phenotypic trait of interest according to claim 10, wherein said nucleic acid molecule associated with said phenotypic trait is located between about 5 and about 10 cM of one or more of said polymorphisms.

16.   (Once Amended) The method of [identifying] isolating a nucleic acid molecule associated with a phenotypic trait of interest according to claim [15] 10, wherein said nucleic acid molecule associated with said phenotypic trait is located between about 0 and about 5cM of one or more of said polymorphisms.

17.   (Once Amended) A method of [isolating] <u>identifying</u> a nucleic acid molecule

associated with a phenotypic trait comprising:

(A)   screening a mapping population of *Arabidopsis* plants to determine the linkage of said

phenotypic trait with a collection of polymorphisms<u>, where the polymorphisms are distributed</u>

<u>throughout the genome of said mapping population of *Arabidopsis* plants at an average density</u>

<u>of more than one polymorphism per about 100 kb</u> [, wherein said at least one polymorphism is

selected from Table A]; and

(B)   <u>identifying</u> [isolating] said nucleic acid molecule associated with said phenotypic

trait based on its linkage to one or more of said polymorphisms.